FIG. 1

Human NRSF Amino Acid Sequence

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAP
QLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVGDNNFSDSEEGEGLEESADIKGE
PHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRC
DRCGYNTNRYDHYTAHLKHHTRAGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVY
TCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKC
DQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCP
VCDYAASKKCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQ
TKIKGDVAGKKNEKSVKAEKRDVSKEKKPSNNVSVIQVTTRTRKSVTEVKEMDVHTGS
NSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPKGDSKVE
ENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKG
PVQVELPPPMEHAQMEGAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVL
AHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAPMQVVQKEPVQMELSPPMEVV
QKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPP
PPREPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVS
TEDLSPPSPPLPKENLREEASGDQKLLNTGEGNKEAPLQKVGAEEADESLPGLAANIN
ESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLTGINSTVEEPVSP
MLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDS
GLHGARPVPQESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYY LEEAAQGQE

FIG. 2

Human NRSF cDNA sequence

1 ggcggcggcg gcggcgcgga ctgggtgcgc ggcgcagcgt cctgtgttgg aatgtgcggc 61 tgccgcgagc tcgcggcgca gcagcggagc gagcgccgcc gaggcccggg gccccagacc 121
ctggcggcgg ctgcggcagc cgagacggca gggcgaggcc cggaggcctg agcaccctct 181 gcagccccac tcctgggcct tcttggtcca cgacggcccc agcacccaac tttaccaccc 241 tcccccacct
ctccccсgaa actccagcaa caaagaaaag tagtcggaga aggagcggcg 301 actcagggtc gcccgcccct cctcaccgag gaaggccgaa tacagttatg gccacccagg 361 taatggggca gtcttctgga
ggaggagggc tgtttaccag cagtggcaac attggaatgg 421 ccctgcctaa cgacatgtat gacttgcatg acctttccaa agctgaactg gccgcacctc 481 agcttattat gctggcaaat gtggccttaa
ctggggaagt aaatggcagc tgctgtgatt 541 acctggtcgg tgaagaaaga cagatggcag aactgatgcc ggttggggat aacaactttt 601 cagatagtga agaaggagaa ggacttgaag agtctgctga
tataaaaggt gaacctcatg 661 gactggaaaa catggaactg agaagtttgg aactcagcgt cgtagaacct cagcctgtat 721 ttgaggcatc aggtgctcca gatatttaca gttcaaataa agatcttccc cctgaaacac
781 ctggagcgga ggacaaaggc aagagctcga agaccaaacc ctttcgctgt aagccatgcc 841 aatatgaagc agaatctgaa gaacagtttg tgcatcacat cagagttcac agtgctaaga 901 aatttttgt
ggaagagagt gcagagaagc aggcaaaagc cagggaatct ggctcttcca 961 ctgcagaaga gggagatttc tccaagggcc ccattcgctg tgaccgctgc ggctacaata 1021 ctaatcgata tgatcactat
acagcacacc tgaaacacca caccagagct ggggataatg 1081 agcgagtcta caagtgtatc atttgcacat acacaacagt gagcgagtat cactggagga 1141 aacatttaag aaaccatttt ccaaggaaag
tatacacatg tggaaaatgc aactattttt 1201 cagacagaaa aaacaattat gttcagcatg ttagaactca tacaggagaa cgcccatata 1261 aatgtgaact ttgtccttac tcaagttctc agaagactca tctaactaga
catatgcgta 1321 ctcattcagg tgagaagcca tttaaatgtg atcagtgcag ttatgtggcc tctaatcaac 1381 atgaagtaac ccgccatgca agacaggttc acaatgggcc taaacctctt aattgcccac 1441
actgtgatta caaaacagca gatagaagca acttcaaaaa acatgtagag ctacatgtga 1501 acccacggca gttcaattgc cctgtatgtg actatgcagc ttccaagaag tgtaatctac 1561 agtatcactt
caaatctaag catcctactt gtcctaataa aacaatggat gtctcaaaag 1621 tgaaactaaa gaaaaccaaa aaacgagagg ctgacttgcc tgataatatt accaatgaaa 1681 aaacagaaat agaacaaaca
aaaataaaag gggatgtggc tggaaagaaa aatgaaaagt 1741 ccgtcaaagc agagaaaaga gatgtctcaa aagagaaaaa gccttctaat aatgtgtcag 1801 tgatccaggt gactaccaga actcgaaaat
cagtaacaga ggtgaaagag atggatgtgc 1861 atacaggaag caattcagaa aaattcagta aaactaagaa aagcaaaagg aagctggaag 1921 ttgacagcca ttctttacat ggtcctgtga atgatgagga
atcttcaaca aaaaagaaaa 1981 agaaggtaga aagcaaatcc aaaaataata gtcaggaagt gccaaagggt gacagcaaag 2041 tggaggagaa taaaaagcaa aatacttgca tgaaaaaaag tacaaagaag
aaaactctga 2101 aaaataaatc aagtaagaaa agcagtaagc ctcctcagaa ggaacctgtt gagaagggat 2161 ctgctcagat ggaccctcct cagatggggc ctgctcccac agaggcggtt cagaaggggc
2221 ccgttcaggt ggagctgcca cctcccatgg agcatgctca gatggagggt gcccagatac 2281 ggcctgctcc tgacgagcct gttcagatgg aggtggttca ggaggggcct gctcagaagg 2341
agctgctgcc tcccgtggag cctgctcaga tggtgggtgc ccaaattgta cttgctcaca 2401 tggagctgcc tcctcccatg gagactgctc agacggaggt tgcccaaatg gggcctgctc 2461 ccatggaacc
tgctcagatg gaggttgccc aggtagaatc tgctcccatg caggtggtcc 2521 agaaggagcc tgttcagatg gagctgtctc ctcccatgga ggtggtccag aaggagcctg 2581 ttcagataga gctgtctcct
cccatggagg tggtccagaa ggaacctgtt aagatagagc 2641 tgtctcctcc catagaggtg gtccagaagg agcctgttca gatggagttg tctcctccca 2701 tgggggtggt tcagaaggag cctgctcaga
gggagccacc tcctcccaga gagcctcccc 2761 ttcacatgga gccaatttcc aaaaagcctc ctctccgaaa agataaaaag gaaaagtcta 2821 acatgcagag tgaaagggca cggaaggagc aagtccttat
tgaagttggc ttagtgcctg 2881 ttaaagatag ctggcttcta aaggaaagtg taagcacaga ggatctctca ccaccatcac 2941 caccactgcc aaaggaaaat ttaagagaag aggcatcagg agaccaaaaa
ttactcaaca 3001 caggtgaagg aaataaagaa gcccctcttc agaaagtagg agcagaagag gcagatgaga 3061 gcctacctgg tcttgctgct aatatcaacg aatctaccca tatttcatcc tctggacaaa 3121
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accagtttca ccaatgcttc ccccttcagc agtagaagaa cgtgaagcag 3301 tgtccaaaac tgcactggca tcacctcctg ctacaatggc agcaaatgag tctcaggaaa 3361 ttgatgaaga tgaaggcatc
cacagccatg aaggaagtga cctaagtgac aacatgtcag 3421 agggtagtga tgattctgga ttgcatgggg ctcggccagt tccacaagaa tctagcagaa 3481 aaaatgcaaa ggaagccttg gcagtcaaag
cggctaaggg agatttgtt tgtatcttct 3541 gtgatcgttc tttcagaaag ggaaaagatt acagcaaaca cctcaatcgc catttggtta 3601 atgtgtacta tcttgaagaa gcagctcaag ggcaggagta atgaaacttt
gaacaaggtt 3661 tca

FIG. 3

Mouse NRSF Amino Acid Sequence

MATQVMGQSSGGGSLFNNSANMGMALTNDMYDLHELSKAELAAP
QLIMLANVALTGEASGSCCDYLVGEERQMAELMPVGDNHFSESEGEGLEESADLKGLE
NMELGSLELSAVEPQPVFEASAAPEIYSANKDPAPETPVAEDKCRSSKAKPFRCKPCQ
YEAESEEQFVHHIRIHSAKKFFVEESAEKQAKAWESGSSPAEEGEFSKGPIRCDRCGY
NTNRYDHYMAHLKHHLRAGENERIYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCSKC
NYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCDQCNY
VASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYA
ASKKCNLQYHFKSKHPTCPSKRMDVSKVKLKKTKKREADLLNNAVSNEKMENEQTKTK
GDVSGKKNEKPVKAVGKDASKEKKPGSSVSVVQVSTRTRKSAVAAETKAAEVKHTDGQ
TGNNPEKPCKAKKNKRKKDAEAHPSEEPVNEGPVTKKKKKSECKSKISTNVPKGGGRA
EERPGVKKQSASLKKGTNKTPPKTKTSKKGGKLAPKGMGQTEPSSGALAQVGVSPDPA
LIQAEVTGSGSSQTELPSPMDIAKSEPAQMEVSLTGPPPVEPAQMEPSPAKPPQVEAP
TYPQPPQRGPAPPTGPAPPTGPAPPTEPAPPTGLAEMEPSPTEPSQKEPPPSMEPPCP
EELPQAEPPPMEDCQKELPSPVEPAQIEVAQTAPTQVQEEPPPVSEPPRVKPTKRSSL
RKDRAEKELSLLSEMARQEQVLMGVGLVPVRDSKLLKGNKSAQDPPAPPSPSPKGNSR
EETPKDQEMVSDGEGTIVFPLKKGGPEEAGESPAELAALKESARVSSSEQNSAMPEGG
ASHSKCQTGSSGLCDVDTEQKTDTVPMKDSAAEPVSPPTPTVDRDAGSPAVVASPPIT
LAENESQEIDEDEGIHSHDGSDLSDNMSEGSDDSGLHGARPTPPEATSKNGKAGLAGK
VTEGEFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEEAAEEQEEQEEREEQE

FIG. 4

Mouse NRSF cDNA

atggccaccc aggtgatggg gcagtcttct ggaggaggca gtctcttcaa caacagtgcc 61 aacatgggca tggccttaac caacgacatg tacgacctgc acgagctctc gaaagctgaa 121
ctggcagccc ctcagctcat catgttagcc aacgtggccc tgacggggga ggcaagcggc 181 agctgctgcg attacctggt cggtgaagag aggcagatgg ccgaattgat gcccgtggga 241
gacaaccact tctcagaaag tgaaggagaa ggcctggaag agtcggctga cctcaaaggg 301 ctggaaaaca tggaactggg aagtttggag ctaagtgctg tagaacccca gcccgtattt 361
gaagcctcag ctgccccaga aatatacagc gccaataaag atcccgctcc agaaacaccc 421 gtggcggaag acaaatgcag gagttctaag gccaagccct tccggtgtaa gccttgccag 481
tacgaagccg aatctgaaga gcagtttgtg catcacatcc ggattcacag cgctaagaag 541 ttctttgtgg aggaaagtgc agagaaacag gccaaagcct gggagtcggg gtcgtctccg 601
gccgaagagg gcgagttctc caaaggcccc atccgctgtg accgctgtgg atacaatacc 661 aaccggtatg accactacat ggcacacctg aagcaccacc tgcgagctgg cgagaacgag 721
cgcatctaca agtgcatcat ctgcacgtac acgacggtca gcgagtacca ctggaggaaa 781 cacctgagaa accatttccc caggaaagtc tacacctgca gcaagtgcaa ctacttctca 841
gacagaaaaa ataactacgt tcagcacgtg cgaactcaca caggagaacg cccgtataaa 901 tgtgaacttt gtccttactc aagctctcag aagactcatc taacgcgaca catgcggact 961
cattcaggtg agaagccatt taaatgtgat cagtgcaatt atgtggcctc taatcagcat 1021 gaagtgaccc gacatgcaag acaggttcac aacgggccta aacctcttaa ttgcccgcac 1081
tgtgactaca aaacagcaga tagaagcaac ttcaaaaagc acgtggagct gcatgttaac 1141 ccacggcagt tcaactgccc cgtgtgtgac tacgcggctt ctaagaagtg taatctacaa 1201
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aagatggaga atgagcaaac aaaaacaaag gggatgtgt ctgggaagaa gaacgagaaa 1381 cctgtaaaag ctgtgggaaa agatgcttca aaagagaaga agcctggtag cagtgtctca 1441
gtggtccagg taagtaccag gactcggaag tcagcggtgg cggcggagac taaagcagca 1501 gaggtgaaac acacagacgg acaaacagga aacaatccag aaaagccctg taaagccaag
1561 aaaaacaaaa gaaagaagga tgctgaggcc catccctccg aagagcctgt gaacgaggga 1621 ccagtgacaa aaaagaaaaa gaagtctgag tgcaaatcaa aaatcagtac caacgtgcca
1681 aagggcggcg gccgagcgga ggagaggccg gggtcaaga agcaaagcgc ttcccttaag 1741 aaaggcacaa ataagacgcc gcccaagaca aagacaagta aaaaaggtgg
caaacttgct 1801 ccaaagggga tggggcagac agaaccttct tctggggcat tggctcaagt gggggtgtct 1861 ccagaccctg ccctcattca ggcagaggtc accgggtcag gatcttctca
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gctgccttct 2281 cccgtggagc ccgctcagat tgaggttgct cagacggccc ctacgcaggt tcaggaggag 2341 ccccctcctg tctcggagcc acctcgggtg aagccaacca aaagatcatc
tctccggaaa 2401 gacagagcag agaaggagct gagcctgctg agtgagatgg cgcggcagga gcaggtcctc 2461 atgggggttg gcttggtgcc tgttagagac agcaagcttc tgaagggaaa
caagagcgcc 2521 caggaccccc cagccccacc gtcaccatcg ccaaagggaa actcgaggga agagacaccc 2581 aaggaccaag aaatggtctc tgatggggaa ggaactatag tattccctct
caagaaagga 2641 ggaccagagg aagctggaga gagtccagct gagttggctg ctctcaagga gtctgcccgt 2701 gtttcatcct ctgaacaaaa ctcagccatg ccagagggtg gagcatcaca
cagcaagtgt 2761 cagactggct cctctgggct ttgtgacgtg gacactgagc agaagacaga tactgtcccc 2821 atgaaagact ccgcagcaga gccagtgtcc cctcctaccc caacagtgga
ccgtgacgca 2881 gggtcaccag ctgtagtggc ctcccctcct atcacgttgg ctgaaaacga gtctcaggaa 2941 attgatgaag atgaaggcat ccatagccat gatggaagtg acctgagtga
caacatgtct 3001 gaggggagtg acgactcagg actgcacggg gctcggccga caccaccaga agctacgtca 3061 aaaaatggga aggcagggtt ggctggtaaa gtgactgagg gagagtttgt
gtgtattttc 3121 tgtgatcgtt cttttagaaa ggaaaaagat tatagcaaac acctcaatcg ccacttggtg 3181 aatgtgtact tcctagaaga agcagctgag gagcaggagg agcaggagga
gcgggaggag 3241 caggagtag

FIG. 5

Rat NRSF Amino Acid Sequence

MATQVMGQSSGGGSLFNNSGNMGMALPNDMYDLHDLSKAELAAP
QLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVGDNHFSDSEGEGLEESAELKGDP
SGLDNMELRSLELSVVEPQPVFEASAAPEVYSSNKDPAPEAPVAEDKCKNLKAKPFRC
KPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGASPSEEGEFSKGPIRCD
RCGYNTNRYDHYTAHLKHHLRAGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYT
CSKCNYFSTEKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCD
QCNYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPV
CDYAASKKCNLQYHFKSKHPTCPSKTMDVSKVKLKKTKRREADLHRDAAAAATEQTDT
EQAKTKGVDASARRSERPVKGVGKDVPKEKKPCSNASVVQVTTRTRKSAVETKAAEGK
HTDGQTGNNAEKSSKAKKSKRKMDAEAHPSVEPVTEGPVTKKKKTESKPKTSGEVPKG
SRVEDRKADKQQSASIKKGGKKTALKTKTAKKGSKLAPKWVGHTEPSSEMAQGGESPV
PALTQAVVTPSGSTQTELSSPMDIAQTEPAQMDVSQTGPPQVQRPLPVEPAQLEPSPP
QEPPQVEPPACVEPPPPVEPPCPMEPAEMEPSPPMEPSQVEPPPHLEPPLPMELPQVE
LPPVEDCQKELPPVEHAQTKVAQTGPTQVGAVQEEPLFCLRATSSQANQKVISPKDRA
KEKLSVLSEMARQEQVLIEVGLVPVRDSQLLKASKSAPDLPAPPSPLPKGHLRREETP
KDQEMFSDGEGNKVSPLEKGGTEEAGESRAELAAPMESTSALSSEQSSNAPDGETLHS
ECQADSTAVCEMEVDTEQKTDRVPLKDSAVEPVSPLNPRVDPEAAAPAVVASPPITLA
ESQEIDEDEGIHSHDGSDLSDNMSEGSDDSGLHGARPAPQEATSKSGKEGLAVKVTEG
EFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEEAAEEQ

FIG. 6

Rat NRSF cDNA Sequence

atggccaccc aggtgatggg gcagtcttct ggaggaggaa gtctctttaa caacagtggc 61 aacatgggca tggccttacc caacgacatg tatgacttgc acgacctctc gaaagctgaa 121
ctggcggcac ctcagctcat tatgttagcc aacgtggccc tgactgggga agtgaatggc 181 agctgctgtg attacctggt tggtgaagag agacagatgg ccgagttgat gcctgttgga
241 gacaaccact tttcagatag cgaaggagaa ggccttgagg agtcggctga actaaaaggt 301 gaccccagtg ggctggacaa catggaactg agaagtttgg agctaagcgt
tgtagagccc 361 cagcccgtat ttgaagcatc agctgcccca gaagtgtaca gctcgaataa agatcccgcc 421 cctgaagcac ccgtggcgga ggacaaatgc aagaatttga
aggccaaacc cttccgttgt 481 aagccatgcc agtatgaagc ggagtctgaa gaacagttcg tacatcacat ccgggttcac 541 agtgctaaga agttttttgt ggaagagagt
gcagagaagc aagccaaagc cagggaatct 601 ggggcttccc cgtctgagga gggcgagttc tccaagggtc ccatccgctg tgatcgctgt 661 ggctacaata ccaaccggta
tgatcactac acggcacacc tgaagcacca cctgagagcc 721 ggggataacg agcgtgtcta caagtgtatc atttgcacgt acacgacagt cagcgaatac 781 cactggcgga
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acgaagtgac ccgacacgca agacaggttc acaacgggcc taaacctctt 1081 aattgccctc actgtgacta caaaacagcc gataggagca acttcaagaa gcacgtcgag 1141
ctgcacgtca accctcggca gttcaactgc cccgtgtgtg actacgcggc ctccaagaag 1201 tgtaacctgc agtaccattt caagtccaag caccccacct gccccagcaa gacgatggac
1261 gtgtccaaag tgaagctgaa gaaaaccaag aggagggagg ctgacctgca ccgtgacgcc 1321 gccgccgccg ccactgagca gacggacaca gagcaagcga aaaccaaggg
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atggacgccg aggcccatcc ctcggtcgag 1621 cctgtgactg agggacccgt gacaaagaag aaaaagacgg agagcaaacc caagaccagc 1681 ggcgaagtgc cgaagggcag
cagagtggag gacaggaagg cggacaaaca gcaaagtgct 1741 tccattaaga aaggcgggaa gaagacggct ctcaagacta agacagctaa aaaaggcagc 1801 aaacttgctc
cgaagtgggt ggggcacaca gaaccttcct cggagatggc tcaaggaggg 1861 gagtctccag ttcctgctct cactcaggcg gtggtcaccc catcaggatc tactcagaca 1921
gagctctctt ctcccatgga tattgctcag acagagcctg cccagatgga cgtttcccag 1981 acagggccgc ctcaggtgca gcggcctctt cctgtggagc ctgctcaatt ggagccgtct
2041 cctcctcagg agcctcccca ggtagagcca cctgcctgtg tggagcctcc ccctcccgtg 2101 gagcctccat gtcccatgga gcctgctgag atggaaccgt cccctcccat
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gcttctgaag gccagcaaga gcgcaccgga cctcccagcc 2521 ccaccgtcac cactgccaaa gggacacttg agaagagaag agacacccaa ggaccaagaa 2581 atgttctctg
acggggaagg aaataaagta tcccctctcg agaaaggagg aacagaggaa 2641 gctggtgaga gtcgagctga gctggctgct cccatggaat ctaccagtgc tttatcctct 2701
gaacaaagct caaatgcacc agatggtgaa acattacaca gcgagtgtca ggctgactcc 2761 actgcggttt gtgaaatgga agtggacact gagcagaaga cagaccgtgt ccctctgaaa
2821 gactcagcag tagaaccagt gtcacctctt aacccaagag tggaccctga agcagcggca 2881 ccagctgtgg tggcctcccc tcctatcact ttggccgagt ctcaggaaat
tgatgaggat 2941 gaaggcattc acagccatga tggaagtgac ctgagcgaca acatgtctga ggggagtgat 3001 gactcaggac tgcatggggc tcggccagca ccacaggaag
ctacgtcaaa aagtggaaag 3061 gaagggttgg ctgtcaaagt aactgaggga gagtttgttt gtatttttttg tgatcgttct 3121 tttagaaagg aaaaagacta tagcaaacac ctcaatcgcc
atttggttaa tgtgtacttc 3181 cttgaagaag cagctgagga gcaggagtag agtagctgat cctcgaggag aagcgcaatg 3241 cgactttgta a

FIG. 7

Xenopus NRSF partial Amino Acid Sequence

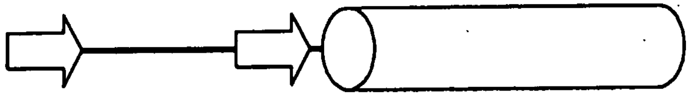
MATQMVNQSTGNSLFCTSTYSNISLDNDMYGLHDLSKADMAAPR
LIMLANVALTGELSSGCCDYTPEGERQMAELTTVNDNSFSDSEGDRLEDSPSMDIQSH
NFIMEMEPAECSKEGTSENDGTLLSNTLEVEVQKDKRTPSPTDDKYKCVKSKPFRCKP
CQYKAESEEEFVHHIKIHSAKIYVDNDSNKKAQGNEADSSISEESDVSKGPIQCDRCG
YNTNRFDHYLAHLKHHNKAGENERVYKCTICTYTTVSEYHWKKHLRNHYPRILYTCSQ
CSYFSDRKNNYIQHIRTHTGERPYQCILCPYSSSQKTHLTRHMRTHSGEKPFKCEQCS
YVASNQHEVTRHARQVHNGPKPLTCPHCDYKTADRSNFKKHVELHVNPRQFLCPVCDY
AASKKCNLQYHIKSRHSGCTNITMDVSKVKLRTKKGDIGVADVDANKQTENGNIIDKS
VEETVKAEKRESCGKAKKSIVNLVDGQVAKKRRLSSTQKKIKTSDARPEKILDKSRKS
SCVKRKSDLLENSNDTQTSTV

FIG. 8

Xenopus NRSF partial cDNA sequence

```
   1 ggcacgagca gtcggttgag acgccgattt gagaaccgtg gacagttctt gaatttggga
  61 gggagaatgg cgcaagtgtg cgaccggatt cccgaaaagt tataaacatg gccactcaaa
 121 tggtcaacca gtctacaggt aacagcttgt tctgtaccag cacctactcc aatatttcat
 181 tggacaatga catgtatggg ttgcatgacc tttcaaaagc tgatatggca gcccctcgat
 241 tgataatgct agcaaatgtg gctctgactg gcgaactcag tagtggttgc tgtgattaca
 301 cgccagaagg agaaaggcaa atggcagaac taacaactgt aaatgacaac agcttctcag
 361 atagtgaggg ggataggttg gaagattcac ccagcatgga tattcagtca cacaatttta
 421 taatggagat ggagccagct gaatgttcaa aagaaggaac gtctgaaaat gatggaactc
 481 tactctctaa tacacttgag gtggaggttc aaaaggataa aaggacaccc agcccaacag
 541 atgacaaata caaatgtgtg aaaagcaaac catttcggtg caaaccttgt cagtacaaag
 601 cagagtctga agaagaattt gttcatcaca ttaagattca cagcgctaag atatatgttg
 661 ataatgactc aaataaaaaa gcgcagggta atgaggcaga ttctagcata tcggaggaat
 721 ctgatgtctc caaaggacct attcagtgtg acaggtgtgg atacaataca aatcgttttg
 781 atcactatct ggctcattta aagcatcaca acaaagctgg agaaaatgaa agagtataca
 841 aatgtacaat atgtacttat actacagtca gtgaatatca ctggaagaaa catctacgta
 901 accattatcc aaggatactc tatacatgct cacaatgttc ctatttttct gataggaaaa
 961 ataattatat ccagcatata agaacacata caggagaacg accatatcag tgtattctat
1021 gtccttactc aagctcacag aaaacccact tgaccaggca catgcgaact cattcaggtg
1081 agaagccttt caaatgtgag cagtgtagtt atgttgcatc caatcagcat gaagttacac
1141 gtcatgcaag acaggttcac aatggaccaa aaccattaac ttgccctcat tgtgactaca
1201 aaactgcaga tcgcagtaat ttcaagaagc atgtagagtt acatgttaat cctcgacagt
1261 ttctatgccc tgtttgtgac tatgctgctt ccaaaaagtg taacttgcaa tatcatataa
1321 aatccagaca ctcaggatgc acaaatatca caatggatgt ttccaaagta aaactgagga
1381 caaagaaagg agacatagga gttgcagatg ttgatgcaaa taagcaaaca gagaatggaa
1441 atataataga taaatctgtg gaagagaccg ttaaagcaga gaaaagggaa agctgtggga
1501 aagctaaaaa aagtattgtt aatttagttg atggccaggt tgcaaaaaaa aggcgcttgt
1561 catctactca gaaaaaaatt aaaacttcag acgcaaggcc tgaaaagatt ttagataaat
1621 cccgtaagtc tagttgtgtg aaaagaaaat ctgatttatt agaaaattct aatgataccc
1681 aaacaagcac tgtg
```

FIG. 9



```
Zif268 RPYA CPVES CDRRFS RSDELTR HIRI -HTGQK P
         FQ CRI -- CMRNFS RSDHLTT HIRT -HTGEK P
         FA CDI -- CGRKFA RSDERKR HTKI -HLRQKD

NRSF   KPFR CKP -- CQYEAE SEEQFVH HIRV -HSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGP
         IR CDR -- CGYNTN RYDHYTA HLKH -HTRAGDNERV
         YK CII -- CTYTTV SEYHWRK HLRN -HFPRKV
         YTCGK -- CNYFSD RKNNYVQ HVRT -HTGERP
         YK CEL -- CPYSSS QKTHLTR HMRT -HSGEKP
         FK CDQ -- CSYVAS NQHEVTR HARQV HNGPKP
         LN CPH -- CDYKTA DRSNFKK HVEL -HVNPRQ
         FN CPV -- CDYAAS KKCNLQY HFKSK HPTCPN
```

FIG. 10

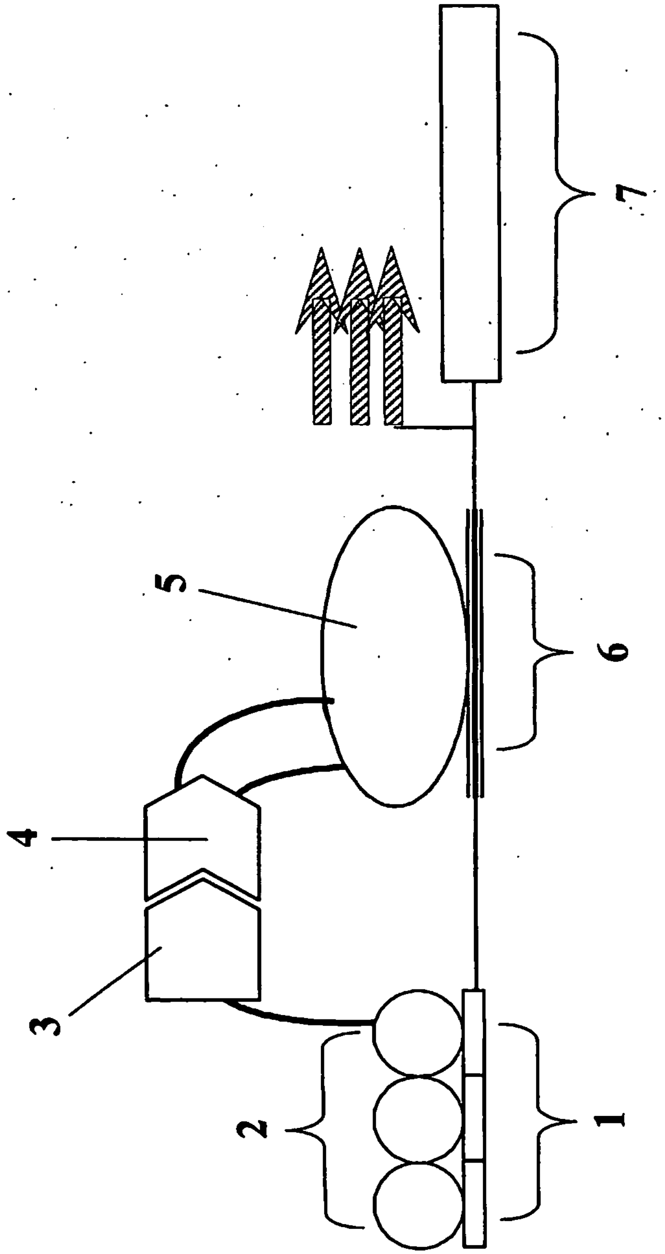


FIG. 11

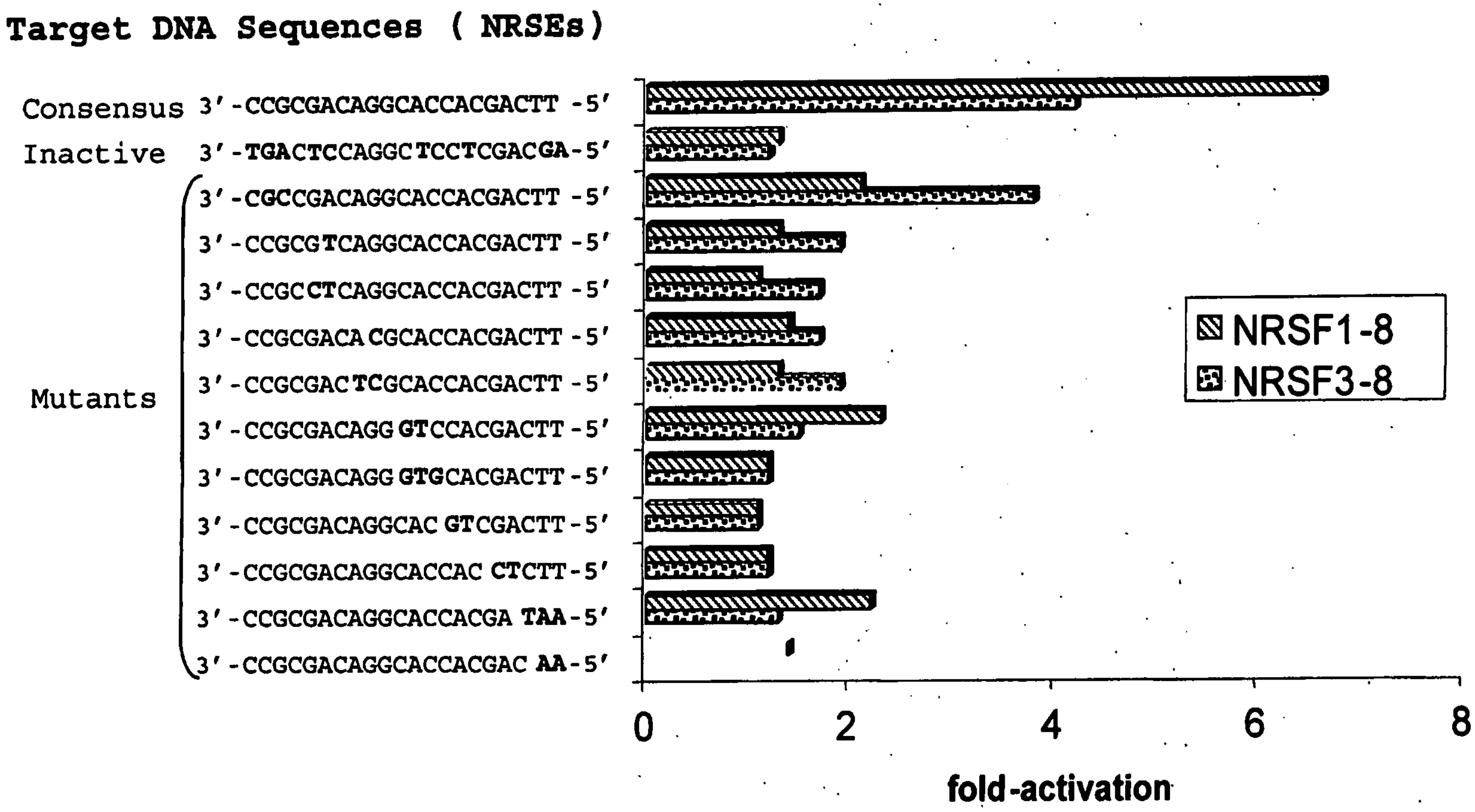

Target DNA Sequences (NRSEs)
Consensus 3'-CCGCGACAGGCACCACGACTT -5'
Inactive 3'-TGACTCCAGGCTCCTCGACGA-5'
Mutants
3'-CGCCGACAGGCACCACGACTT -5'
3'-CCGCGTCAGGCACCACGACTT -5'
3'-CCGCCTCAGGCACCACGACTT -5'
3'-CCGCGACA CGCACCACGACTT -5'
3'-CCGCGACTCGCACCACGACTT -5'
3'-CCGCGACAGG GTCCACGACTT -5'
3'-CCGCGACAGG GTGCACGACTT -5'
3'-CCGCGACAGGCAC GTCGACTT -5'
3'-CCGCGACAGGCACCAC CTCTT -5'
3'-CCGCGACAGGCACCACGA TAA -5'
3'-CCGCGACAGGCACCACGAC AA -5'
▧ NRSF1-8
▨ NRSF3-8
0
2
4
6
8
fold-activation

FIG. 12

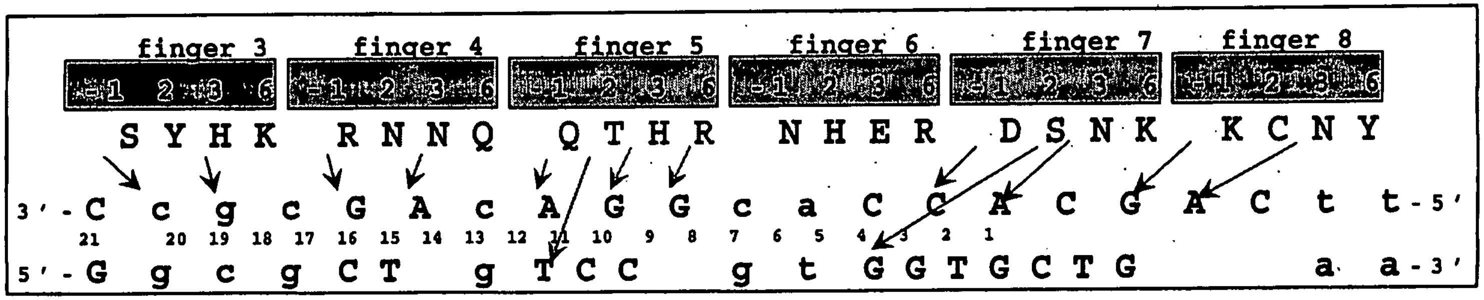

finger 3
finger 4
finger 5
finger 6
finger 7
finger 8
-1 2 3 6
-1 2 3 6
-1 2 3 6
-1 2 3 6
-1 2 3 6
-1 2 3 6
S Y H K R N N Q Q T H R N H E R D S N K K C N Y
3'-C c g c G A c A G G c a C C A C G A C t t-5'
21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
5'-G g c g C T g T C C g t G G T G C T G a a-3'

FIG. 13

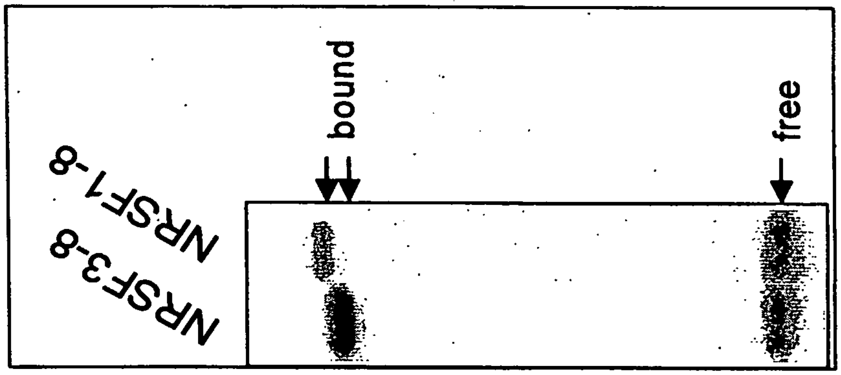


FIG. 14

A. Finger 4 Selections

3'-CCGC**CT**CAGGCACCACGACTT-5'

	-1	1	2	3	5	6
NRSF F4v1	H	K	T	R	M	E
NRSF F4v2	H	K	T	R	M	E
NRSF F4v3	H	K	T	R	M	E
→ NRSF F4v4	H	R	T	R	M	E
NRSF F4v5	H	K	T	R	K	E
NRSF F4v6	H	L	T	R	K	E
NRSF F4v7	H	K	T	R	A	E
→ NRSF F4v8	H	K	T	R	D	E

B. Finger 5 Selections

3'-CCGCGAC**TC**GCACCACGACTT-5'

	-1	1	2	3	5	6
NRSF F5v1	T	V	G	T	R	R
NRSF F5v2	T	R	G	T	K	R
NRSF F5v3	T	G	S	T	R	R
→ NRSF F5v4	T	M	S	G	R	R
NRSF F5v5	T	I	S	A	R	R
→ NRSF F5v6	H	M	P	T	R	R
NRSF F5v7	H	R	G	T	V	R
NRSF F5v8	R	A	P	D	K	R

FIG. 15A

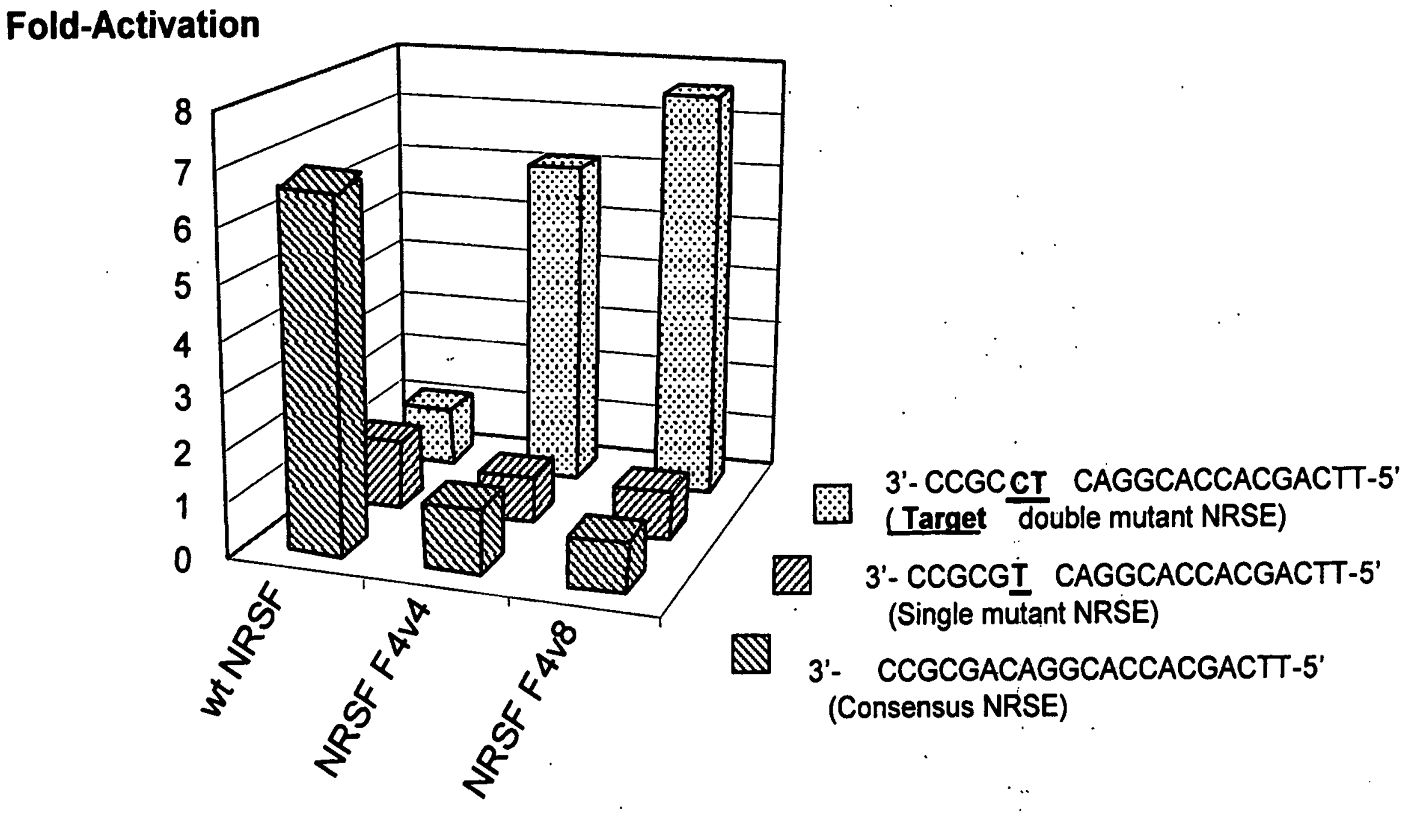

Fold-Activation
8
7
6
5
4
3
2
1
0
wt NRSF
NRSF F4v4
NRSF F4v8
3'- CCGCCT CAGGCACCACGACTT-5'
(Target double mutant NRSE)
3'- CCGCGT CAGGCACCACGACTT-5'
(Single mutant NRSE)
3'- CCGCGACAGGCACCACGACTT-5'
(Consensus NRSE)

FIG. 15B

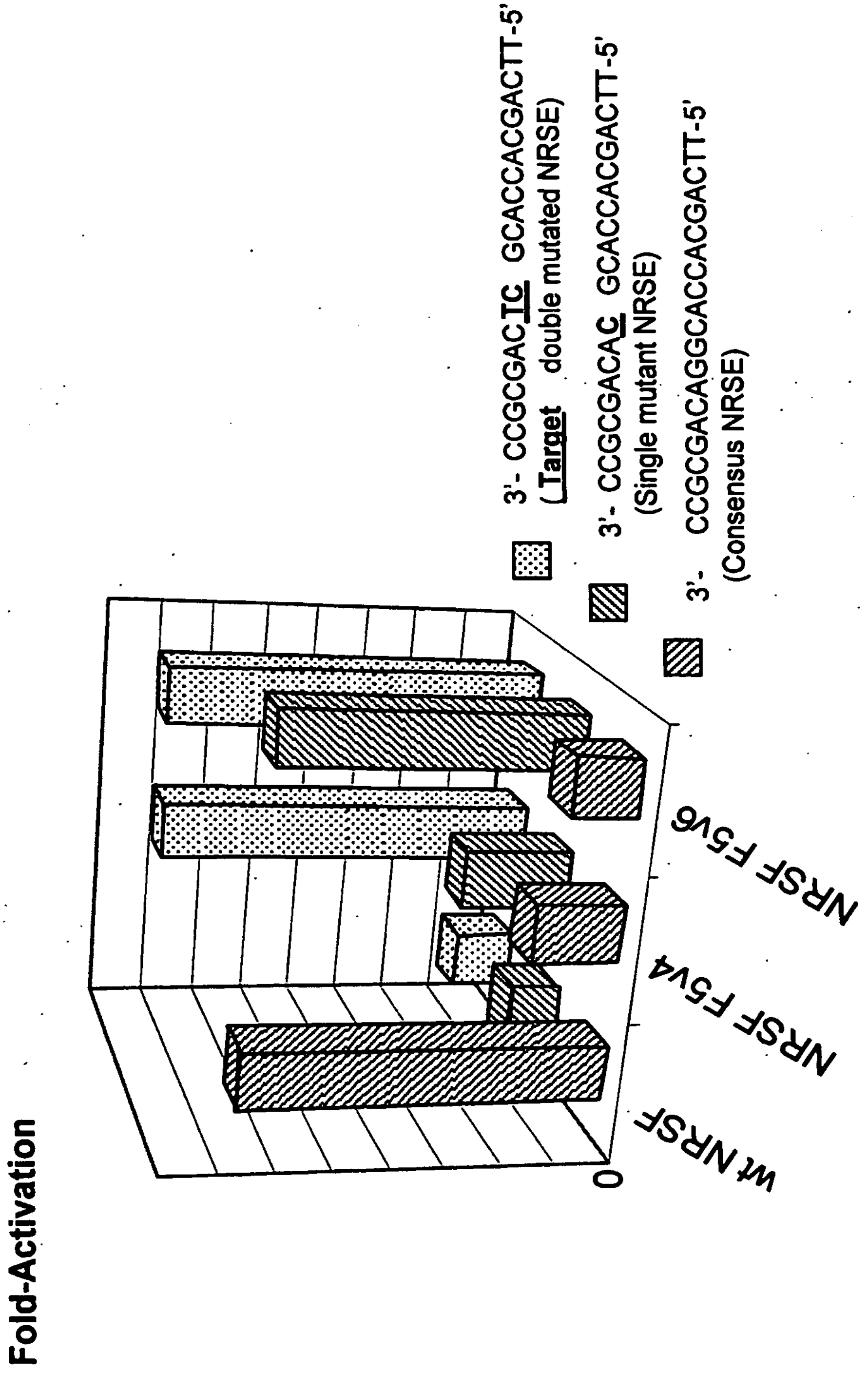

Fold-Activation
0
wt NRSF
NRSF F5V4
NRSF F5V6
3'- CCGCGACTC GCACCACGACTT-5' (Target double mutated NRSE)
3'- CCGCGACAC GCACCACGACTT-5' (Single mutant NRSE)
3'- CCGCGACAGGCACCACGACTT-5' (Consensus NRSE)

FIG. 16

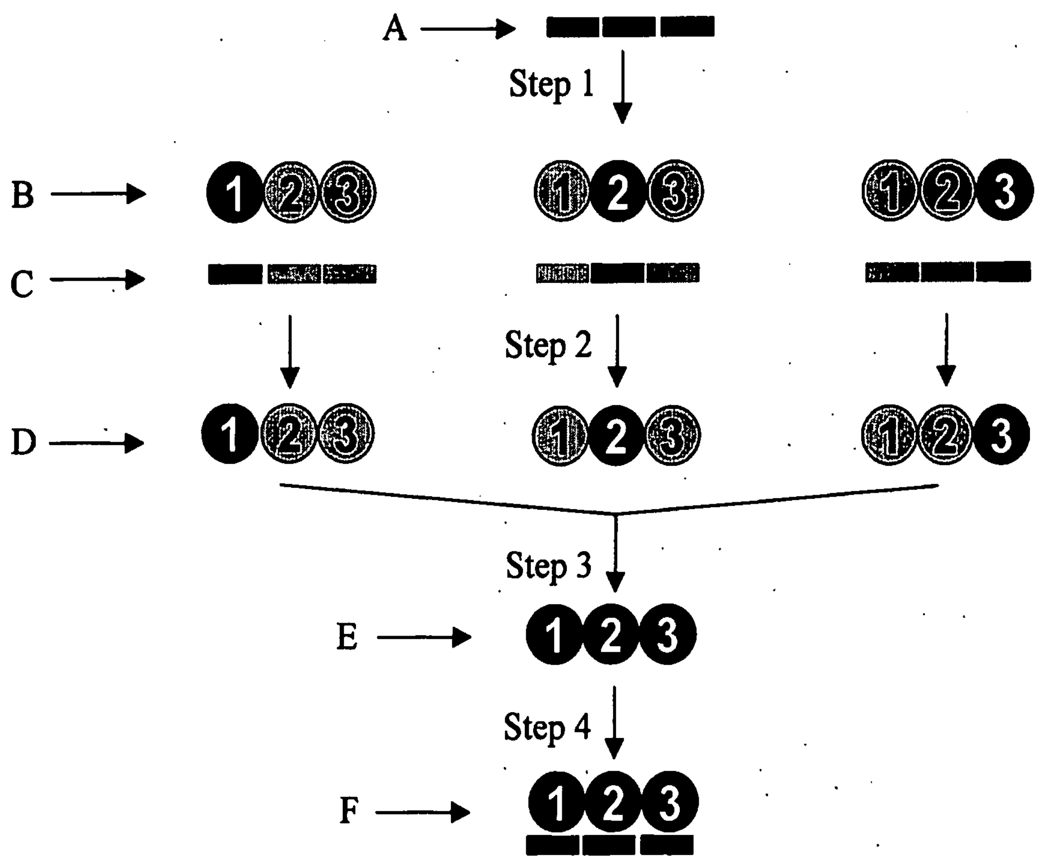


FIG. 17

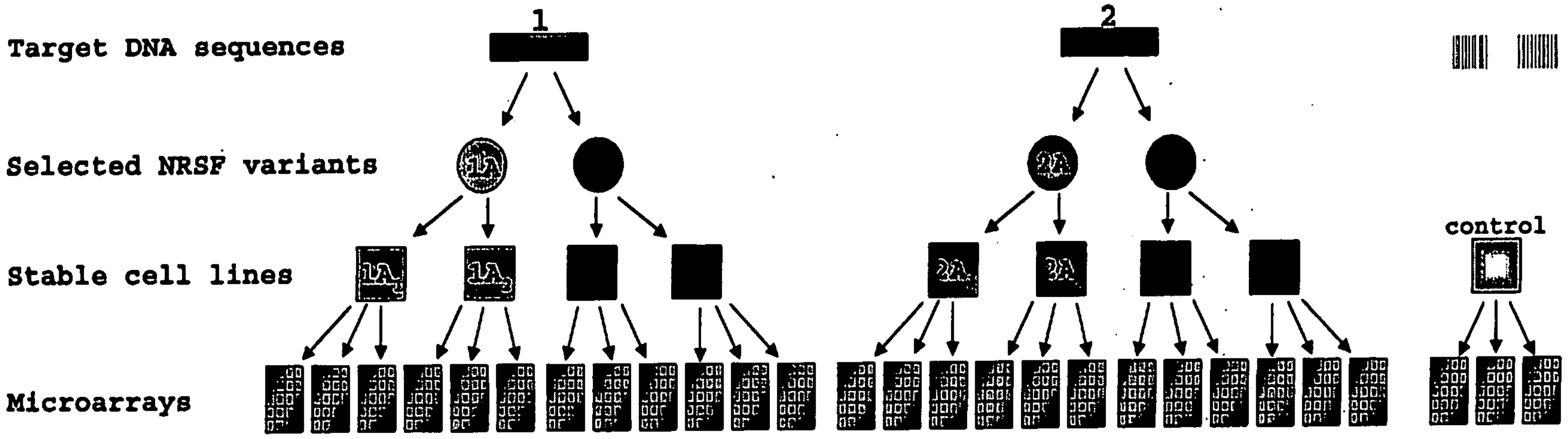

Target DNA sequences
Selected NRSF variants
Stable cell lines
Microarrays
1
2
control
1A
2A
3A

FIG. 18

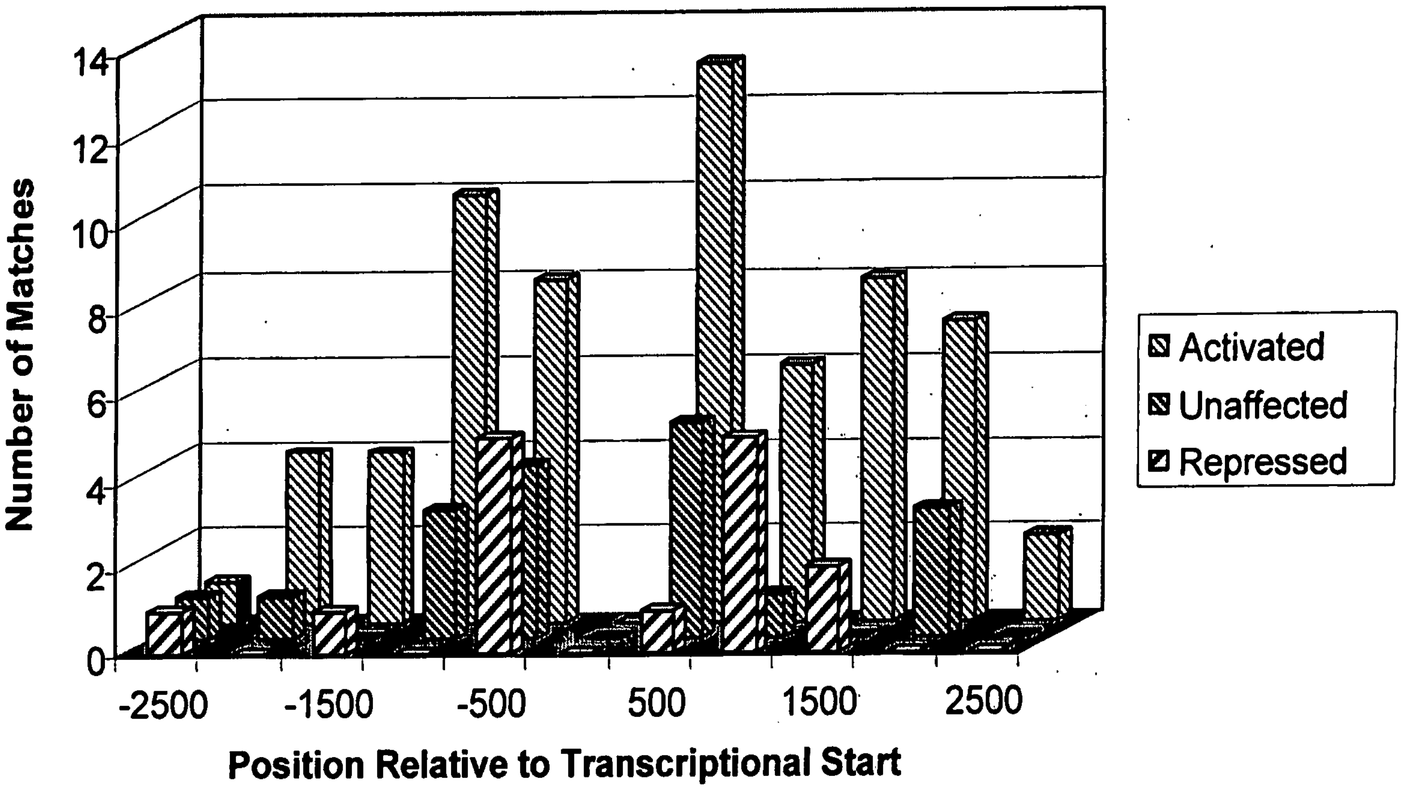

Number of Matches
14
12
10
8
6
4
2
0
-2500
-1500
-500
500
1500
2500
Position Relative to Transcriptional Start
▧ Activated
▧ Unaffected
▨ Repressed

FIG. 19

F4v1 (sequence identical to F4v2, F4v3)

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYME**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 20

F4v4

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDHRTRYMEHVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 21

F4v5

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYKE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 22

F4v6

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HLTRYKE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 23

F4v7

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYAE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
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REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 24

F4v8

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYDE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 25

F5V1

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TVGTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 26

F5v2

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TRGTLK**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 27

F5v3

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TGSTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 28

F5v4

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TMSGLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 29

F5v5

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TISALR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 30

F5v6

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**HMPTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 31

F5v7

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**HRGTLV**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 32

F5v8

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**RAPDLK**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 33

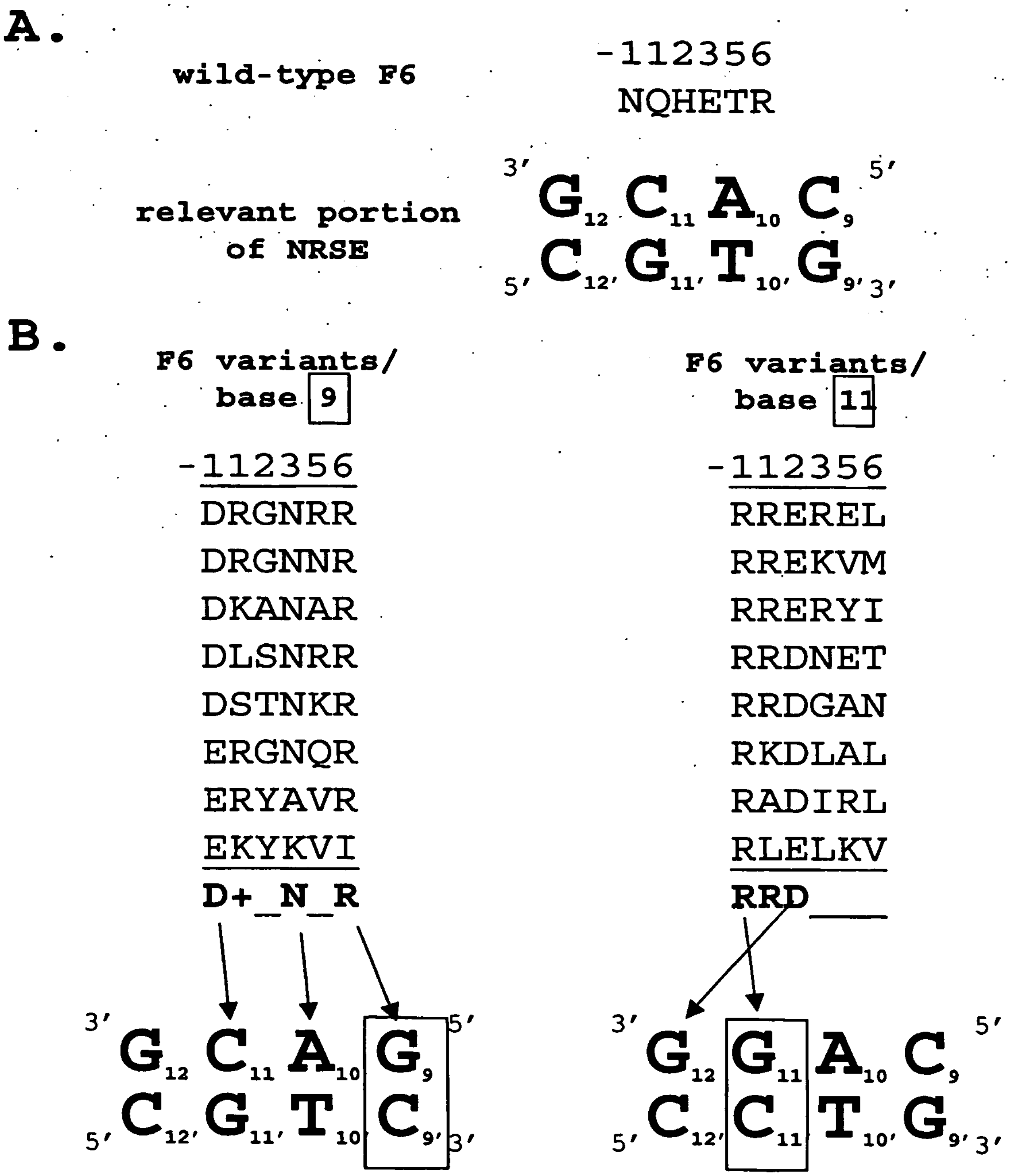

A.
wild-type F6
-112356
NQHETR
relevant portion of NRSE
3′ G12 C11 A10 C9 5′
5′ C12′ G11′ T10′ G9′ 3′
B.
F6 variants/ base 9
-112356
DRGNRR
DRGNNR
DKANAR
DLSNRR
DSTNKR
ERGNQR
ERYAVR
EKYKVI
D+_N_R
3′ G12 C11 A10 G9 5′
5′ C12′ G11′ T10 C9′ 3′
F6 variants/ base 11
-112356
RREREL
RREKVM
RRERYI
RRDNET
RRDGAN
RKDLAL
RADIRL
RLELKV
RRD____
3′ G12 G11 A10 C9 5′
5′ C12′ C11 T10′ G9′ 3′

FIG. 34

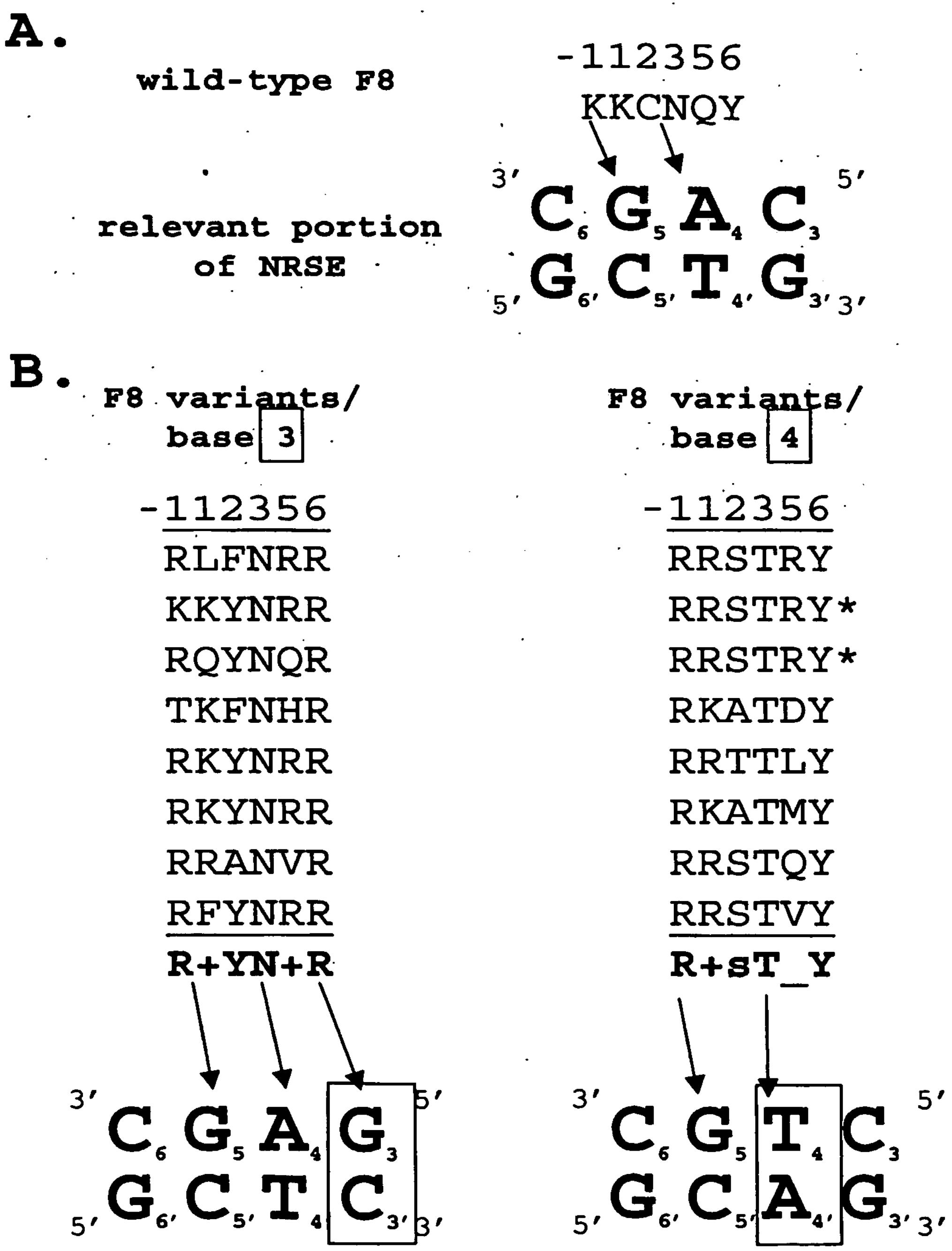
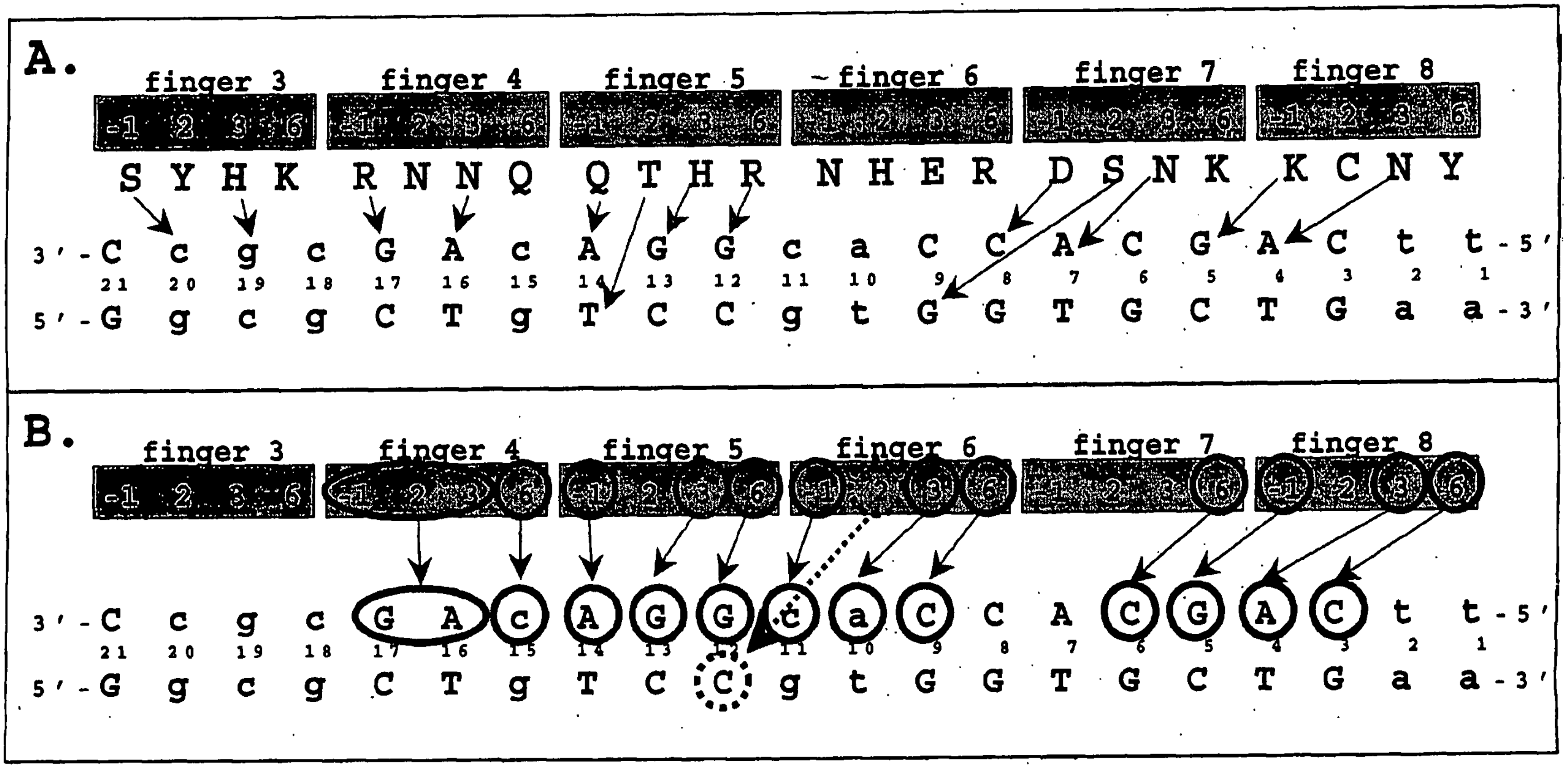

A.
wild-type F8
-112356
KKCNQY
relevant portion of NRSE
3′ C6 G5 A4 C3 5′
5′ G6′ C5′ T4′ G3′ 3′
B.
F8 variants/ base 3
-112356
RLFNRR
KKYNRR
RQYNQR
TKFNHR
RKYNRR
RKYNRR
RRANVR
RFYNRR
R+YN+R
3′ C6 G5 A4 G3 5′
5′ G6′ C5′ T4′ C3′ 3′
F8 variants/ base 4
-112356
RRSTRY
RRSTRY*
RRSTRY*
RKATDY
RRTTLY
RKATMY
RRSTQY
RRSTVY
R+sT_Y
3′ C6 G5 T4 C3 5′
5′ G6′ C5′ A4′ G3′ 3′

FIG. 35


A.
finger 3
finger 4
finger 5
finger 6
finger 7
finger 8
-1 2 3 6
S Y H K R N N Q Q T H R N H E R D S N K K C N Y
3'-C c g c G A c A G G c a C C A C G A C t t-5'
21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
5'-G g c g C T g T C C g t G G T G C T G a a-3'
B.
finger 3
finger 4
finger 5
finger 6
finger 7
finger 8
-1 2 3 6
3'-C c g c G A c A G G c a C C A C G A C t t-5'
21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
5'-G g c g C T g T C C g t G G T G C T G a a-3'